

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lam, Xanthe M.
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5 Ongpipattanakul, Boonsri
Shahrokh, Zahra
Wang, Sharon X.
Weissburg, Robert P.
Wong, Rita L.

10 (ii) TITLE OF INVENTION: Antibody Formulation

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
15 (C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

25 (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

30 (A) APPLICATION NUMBER: 08/874897
(B) FILING DATE: 06/13/1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Lee, Wendy M.
(B) REGISTRATION NUMBER: 40,378
(C) REFERENCE/DOCKET NUMBER: P1089R1

35 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-1994
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
	1				5						10				15
	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Thr	Ser	Gly	Tyr	Thr	Phe	Thr
						20				25					30
10	Glu	Tyr	Thr	Met	His	Trp	Met	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
							35			40					45
	Glu	Trp	Val	Ala	Gly	Ile	Asn	Pro	Lys	Asn	Gly	Gly	Thr	Ser	His
						50			55						60
15	Asn	Gln	Arg	Phe	Met	Asp	Arg	Phe	Thr	Ile	Ser	Val	Asp	Lys	Ser
						65			70						75
	Thr	Ser	Thr	Ala	Tyr	Met	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp
						80				85					90
	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Trp	Arg	Gly	Leu	Asn	Tyr	Gly
						95				100					105
20	Phe	Asp	Val	Arg	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val
						110				115					120
	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu
						125				130					135
25	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly
						140				145					150
	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp
						155				160					165
	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
						170				175					180
30	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
						185				190					195
	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
						200				205					210

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
 215 220 225

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 230 235 240

5 Leu
 241

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 214 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1 5 10 15

15 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asn
 20 25 30

Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 35 40 45

Leu Leu Ile Tyr Tyr Ser Thr Leu His Ser Gly Val Pro Ser
 20 50 55 60

Arg Phe Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
 65 70 75

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 80 85 90

25 Gly Asn Thr Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
 95 100 105

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
 110 115 120

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 30 125 130 135

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 140 145 150

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu

155

160

165

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 170 175 180

5 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
 185 190 195

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
 200 205 210

Arg Gly Glu Cys
 214

10 (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Gly Gly Arg Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu
 1 5 10 15

Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala Arg Leu Lys
 20 25 30

20 Lys Leu Val Gly Glu Arg
 35 36

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro Lys Asn Ser Ser Met Ile Ser Asn Thr Pro
 1 5 10 11

30 (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

His Gln Ser Leu Gly Thr Gln
1 5 7

5 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

His Gln Asn Leu Ser Asp Gly Lys
1 5 8

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 15
- (A) LENGTH: 8 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

His Gln Asn Ile Ser Asp Gly Lys
20 1 5 8

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 25
- (A) LENGTH: 8 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Ile Ser Ser His Leu Gly Gln
1 5 8

(2) INFORMATION FOR SEQ ID NO:9:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2143 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50
 TCATTGCTGA GTTGTATTT AAGCTTGGA GATTATCGTC ACTGCAATGC 100
 5 TTCGCAATAT GCGCAAAAT GACCAACAGC GGTTGATTGA TCAGGTAGAG 150
 GGGCGCTGT ACGAGGTAAA GCCCGATGCC AGCATTCTG ACGACGATAC 200
 GGAGCTGCTG CGCGATTACG TAAAGAAGTT ATTGAAGCAT CCTCGTCAGT 250
 AAAAAGTTAA TCTTTCAAC AGCTGTACATA AAGTTGTCAC GGCCGAGACT 300
 TATAGTCGCT TTGTTTTAT TTTTTAATGT ATTTGTAAC AGAATTGAG 350
 10 CTCGCCGGGG ATCCTCTAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC 400
 GCATTTCTTC TTGCATCTAT GTTCGTTTT TCTATTGCTA CAAACGCGTA 450
 CGCTGATATC CAGATGACCC AGTCCCCGAG CTCCCTGTCC GCCTCTGTGG 500
 GCGATAGGGT CACCATCACC TGTCGTGCCA GTCAGGACAT CAACAATTAT 550
 CTGAACCTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTAA 600
 15 CTATACCTCC ACCCTCCACT CTGGAGTCCC TTCTCGCTTC TCTGGTTCTG 650
 GTTCTGGGAC GGATTACACT CTGACCCTCA GCAGTCTGCA ACCGGAGGAC 700
 TTTCGCAACTT ATTACTGTCA GCAAGGTAAT ACTCTGCCGC CGACGTTCGG 750
 ACAGGGCACG AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT 800
 TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT 850
 20 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA 900
 GGTGGATAAC GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC 950
 AGGACAGCAA GGACAGCACC TACAGCCTCA GCAGCACCT GACGCTGAGC 1000
 AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA 1050
 GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTAAAG 1100

CTGATCCTCT ACGCCGGACG CATCGTGGCG CTAGTACGCA AGTTCACGTA 1150
 AAAACGGTAT CTAGAGGTTG AGGTGATTAT ATGAAAAAAGA ATATCGCATT 1200
 TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG 1250
 AGGTTCAGCT GGTGGAGTCT GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA 1300
 5 CTCCGTTTGT CCTGTGCAAC TTCTGGCTAC ACCTTTACCG AATACACTAT 1350
 GCACTGGATG CGTCAGGCC CGGGTAAGGG CCTGGAATGG GTTGCAGGGA 1400
 TTAATCCTAA AACCGGTGGT ACCAGCCACA ACCAGAGGTT CATGGACCGT 1450
 TTCACTATAA GCGTAGATAA ATCCACCAGT ACAGCCTACA TGCAAATGAA 1500
 CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTATTGTGCT AGATGGCGAG 1550
 10 GCCTGAACTA CGGCTTGAC GTCCGTTATT TTGACGTCTG GGGTCAAGGA 1600
 ACCCTGGTCA CCGTCTCCTC GGCCCTCACC AAGGGCCAT CGGTCTTCCC 1650
 CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT 1700
 GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 1750
 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC 1800
 15 AGGACTCTAC TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG 1850
 GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG 1900
 GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAATC ACACATGCC 1950
 GCCGTGCCCA GCACCAGAAC TGCTGGCGG CCGCATGAAA CAGCTAGAGG 2000
 ACAAGGTCGA AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG 2050
 20 GCAAGACTCA AAAAGCTTGT CGGGGAGCGC TAAGCATGCG ACGGCCCTAG 2100
 AGTCCCTAAC GCTCGGTTGC CGCCGGCGT TTTTTATTGT TAA 2143

(2) INFORMATION FOR SEQ ID NO:10:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 237 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 -23 -20 -15 -10

Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser
 5 -5 1 5

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
 10 15 20

Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln
 25 30 35

10 Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser
 40 45 50

Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
 55 60 65

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 15 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Pro Thr
 85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

20 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
 25 145 150 155

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 160 165 170

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 175 180 185

30 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 190 195 200

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 205 210 214

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 amino acids
 (B) TYPE: Amino Acid
 5 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

	Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe			
	-23	-20	-15	-10
	Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser			
10		-5	1	5
	Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys			
	10	15	20	
	Ala Thr Ser Gly Tyr Thr Phe Thr Glu Tyr Thr Met His Trp Met			
	25	30	35	
15	Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile Asn			
	40	45	50	
	Pro Lys Asn Gly Gly Thr Ser His Asn Gln Arg Phe Met Asp Arg			
	55	60	65	
20	Phe Thr Ile Ser Val Asp Lys Ser Thr Ser Thr Ala Tyr Met Gln			
	70	75	80	
	Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala			
	85	90	95	
	Arg Trp Arg Gly Leu Asn Tyr Gly Phe Asp Val Arg Tyr Phe Asp			
	100	105	110	
25	Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr			
	115	120	125	
	Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr			
	130	135	140	
30	Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe			
	145	150	155	
	Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser			
	160	165	170	
	Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr			

175

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Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
190 195 200

5 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
205 210 215

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
220 225 230

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Arg Met Lys
235 240 245

10 Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His
250 255 260

Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg
265 270 275 277